

## SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> Tyrosine phosphorylation of p27Kip1

<130> 22250

<150> EP03024165.7

<151> 2003-10-20

<160> 25

<170> PatentIn version 3.2

<210> 1

<211> 597

<212> DNA

<213> Homo sapiens

<400> 1

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ttaacccggg acttgagaa gcaactgcaga gacatggaag aggcgagcca gcgcaagtgg      180
aatttcgatt ttcagaatca caaaccccta gagggcaagt acgagtggca agagggtggag      240
aagggcagct tgcccgagtt ctactacaga ccccgcgggc ccccaaagg tgctgcaag      300
gtgccggcgc aggagagcca ggatgtcagc gggagccgcc cggcggcgcc ttaattggg      360
gctccggcta actctgagga cagcatttg gtggaccaa agactgatcc gtcggacagc      420
cagacggggt tagcggagca atgcgcagga ataaggaagc gacctgcaac cgacgattct      480
tctactcaaa acaaagagc caacagaaca gaagaaatg tttcagacgg ttcccaaat      540
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<210> 2

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20           25           30

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Phe Gly Pro Val Asp His Glu Glu Leu Thr Arg Asp Leu Glu Lys His  
 35 40 45

Cys Arg Asp Met Glu Glu Ala Ser Gln Arg Lys Trp Asn Phe Asp Phe  
 50 55 60

Gln Asn His Lys Pro Leu Glu Gly Lys Tyr Glu Trp Gln Glu Val Glu  
 65 70 75 80

Lys Gly Ser Leu Pro Glu Phe Tyr Tyr Arg Pro Pro Arg Pro Pro Lys  
 85 90 95

Gly Ala Cys Lys Val Pro Ala Gln Glu Ser Gln Asp Val Ser Gly Ser  
 100 105 110

Arg Pro Ala Ala Pro Leu Ile Gly Ala Pro Ala Asn Ser Glu Asp Thr  
 115 120 125

His Leu Val Asp Pro Lys Thr Asp Pro Ser Asp Ser Gln Thr Gly Leu  
 130 135 140

Ala Glu Gln Cys Ala Gly Ile Arg Lys Arg Pro Ala Thr Asp Asp Ser  
 145 150 155 160

Ser Thr Gln Asn Lys Arg Ala Asn Arg Thr Glu Glu Asn Val Ser Asp  
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Gly Ser Pro Asn Ala Gly Ser Val Glu Gln Thr Pro Lys Lys Pro Gly  
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Leu Arg Arg Arg Gln Thr  
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tgcattccagg aggcccgtag gcgatggaac ttgcactttg tcaccgagac accactggag 180

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ctgctgcagg ggacagcaga ggaagaccat gtggacctgt cactgtcttg tacccttgtg      360
cctcgctcag gggagcaggc tgaaggggcc ccaggtggac ctggagactc tcagggtcga      420
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<210> 4
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Met Ser Glu Pro Ala Gly Asp Val Arg Gln Asn Pro Cys Gly Ser Lys
1           5           10           15

```

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Ala Cys Arg Arg Leu Phe Gly Pro Val Asp Ser Glu Gln Leu Ser Arg
          20           25           30

```

```

Asp Cys Asp Ala Leu Met Ala Gly Cys Ile Gln Glu Ala Arg Glu Arg
          35           40           45

```

```

Trp Asn Phe Asp Phe Val Thr Glu Thr Pro Leu Glu Gly Asp Phe Ala
          50           55           60

```

```

Trp Glu Arg Val Arg Gly Leu Gly Leu Pro Lys Leu Tyr Leu Pro Thr
65           70           75           80

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Gly Pro Arg Arg Gly Arg Asp Glu Leu Gly Gly Gly Arg Arg Pro Gly
          85           90           95

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Thr Ser Pro Ala Leu Leu Gln Gly Thr Ala Glu Glu Asp His Val Asp
          100          105          110

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Leu Ser Leu Ser Cys Thr Leu Val Pro Arg Ser Gly Glu Gln Ala Glu
          115          120          125

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Gly Ser Pro Gly Gly Pro Gly Asp Ser Gln Gly Arg Lys Arg Arg Gln
          130          135          140

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Thr Ser Met Thr Asp Phe Tyr His Ser Lys Arg Arg Leu Ile Phe Ser  
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Lys Arg Lys Pro

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 gagctgagcc gcgagctgca ggcccgctg gccgagctga acgccgagga ccagaaccgc 180  
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 gaagtggaca gcgactcggg gcccgcttc taccgcgaga cgggtgcaggt ggggcgctgc 300  
 cgcttgcctgc tggcgccgcg gcccgctcgc gtcgcggtgg ctgtcagccc gccctcgag 360  
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20 25 30

Leu Phe Gly Pro Val Asp His Glu Glu Leu Ser Arg Glu Leu Gln Ala  
35 40 45

Arg Leu Ala Glu Leu Asn Ala Glu Asp Gln Asn Arg Trp Asp Tyr Asp  
50 55 60

Phe Gln Gln Asp Met Pro Leu Arg Gly Pro Gly Arg Leu Gln Trp Thr  
65 70 75 80

Glu Val Asp Ser Asp Ser Val Pro Ala Phe Tyr Arg Glu Thr Val Gln  
85 90 95

Val Gly Arg Cys Arg Leu Leu Leu Ala Pro Arg Pro Val Ala Val Ala  
100 105 110

Val Ala Val Ser Pro Pro Leu Glu Pro Ala Ala Glu Ser Leu Asp Gly  
115 120 125

Leu Glu Glu Ala Pro Glu Gln Leu Pro Ser Val Pro Val Pro Ala Pro  
130 135 140

Ala Ser Thr Pro Pro Pro Val Pro Val Leu Ala Pro Ala Pro Ala Pro  
145 150 155 160

Ala Pro Ala Pro Val Ala Ala Pro Val Ala Ala Pro Val Ala Val Ala  
165 170 175

Val Leu Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro  
180 185 190

Ala Pro Val Ala Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro  
195 200 205

Ala Pro Ala Pro Ala Pro Ala Pro Asp Ala Ala Pro Gln Glu Ser Ala  
210 215 220

Glu Gln Gly Ala Asn Gln Gly Gln Arg Gly Gln Glu Pro Leu Ala Asp  
225 230 235 240

Gln Leu His Ser Gly Ile Ser Gly Arg Pro Ala Ala Gly Thr Ala Ala  
245 250 255

Ala Ser Ala Asn Gly Ala Ala Ile Lys Lys Leu Ser Gly Pro Leu Ile  
260 265 270

Ser Asp Phe Phe Ala Lys Arg Lys Arg Ser Ala Pro Glu Lys Ser Ser  
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Gly Ser Val Glu Gln Thr Pro Arg Lys Arg Leu Arg  
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<400> 24

Pro Glu Phe Tyr Tyr Arg Pro Pro  
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<210> 25

<211> 6

<212> PRT

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<400> 25

Glu Phe Tyr Tyr Arg Pro  
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